

**INFORMATION
DISCLOSURE
STATEMENT**

Atty. Docket No.: 265.00400101

Serial No.: 10/817,530

Applicant(s): Braun et al.

Confirmation No.: 4868

Application Filing Date: April 2, 2004

Group: 1631

Information Disclosure Statement mailed:

April 18, 2005**U.S. PATENT DOCUMENTS**

Examiner Initial	Copy Enclosed	Document Number	Date	Name	Class	Subclass	Filing Date If Appropriate
LAC		5,845,049	12/01/98	Wu			
LAC		5,878,373	03/02/99	Cohen et al.			
LAC		6,512,981	01/28/03	Eisenberg et al.			

FOREIGN PATENT DOCUMENTS

Examiner Initial	Copy Enclosed	Document Number	Date	Country	Class	Subclass	Translation	
							Yes	No
		None						

OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

Examiner Initial	Copy Enclosed	Document Description
LAC	X	Altschul et al., "Grapped BLAST and PSI-BLAST: a new generation of protein database search programs," <i>Nucleic Acids Res</i> , 1997;25(17):3389-3402.
	X	Bairoch et al., "The SWISS-PROT protein sequence database and its supplement TrEMBL in 2000," <i>Nucleic Acids Res</i> , 2000;28(1):45-48.
	X	Ben-Hur et al., "Remote homology detection: a motif based approach," <i>Bioinformatics</i> , 2003;19(Suppl. 1):i26-i33.
	X	Benner et al., "Amino acid substitution during functionally constrained divergent evolution of protein sequences," <i>Protein Eng.</i> , 1994;7:1323-1332.
	X	"BLAST." [online]. NCBI Blast.National Institute of Health. [retrieved on 2004-07-06]. Retrieved from the Internet:<http://www.ncbi.nlm.nih.gov/BLAST/>;1 pg.
	X	Bowie et al., "A method to identify protein sequences that fold into a known three-dimensional structure," <i>Science</i> , 1991;253:164-170.
	X	Brenner et al., "The ASTRAL compendium for protein structure and sequence analysis," <i>Nucleic Acids Res.</i> , 2000;28:254-256.
	X	Chandonia et al., "ASTRAL compendium enhancements," <i>Nucleic Acids Res.</i> , 2002;30(1):260-263.
LAC	X	Chothia et al., "The relation between the divergence of sequence and structure in proteins," <i>EMBO J</i> , 1986;5: 823-826.

EXAMINER

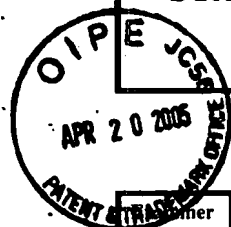
J. A. C. L. C.

Date Considered

11/21/07


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LAC



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LAC	X	"ClustalW." [online]. European Bioinformatics Institute (EMBL-EBI).[retrieved on 2004-07-06]. Retrieved from the Internet:< http://www.ebi.ac.uk/clustalw/ >;2 pgs.
	X	Dubchak et al., "Recognition of a protein fold in the context of the SCOP classification," <i>Proteins</i> , 1999;35:401-407.
	X	Eddy, S.R., "Profile hidden Markov models," <i>Bioinformatics</i> , 1998;14:755-763.
	X	"Emotif Maker." [online]. Biochemistry. Stanford University, Stanford, CA [retrieved on 2004-07-06].Retrieved from the Internet:< http://fold.stanford.edu/emotif/emotif-maker.html >;2 pgs.
	X	Falquet et al., "The PROSITE database, its status in 2002," <i>Nucleic Acids Res</i> , 2002;30: 235-238.
	X	Gough et al., "SUPERFAMILY: HMMs representing all proteins of known structure. SCOP sequence searches, alignments and genome assignments," <i>Nucleic Acids Res</i> , 2002;30: 268-272.
	X	Gribskov et al., "Identification of sequence patterns with profile analysis," <i>Methods Enzymol</i> , 1996;266:198-212.
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	X	Higgins et al., "Multiple sequence alignment," <i>Methods Mol Biol.</i> , 2000;143: 1-18.
	X	Holm et al., "Mapping the protein universe," <i>Science</i> , 2000;273:595-602.
	X	Kelley et al., "Enhanced genome annotation using structural profiles in the program 3D-PSSM," <i>J Mol Biol</i> , 2000;299: 499-520.
	X	Kostich et al., "Human members of the eukaryotic protein kinase family," <i>Genome Biol</i> , 2002;3:43.
	X	Kullback et al., "On information sufficiency," <i>Ann Math Stat</i> , 1951;22: 79-86.
LAC	X	Lo Conte et al., "SCOP database in 2002: refinements accommodates structural genomics," <i>Nucleic Acids Res</i> , 2002;30: 264-267.

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UK	X	Marcotte et al., "A combined algorithm for genome-wide prediction of protein function," <i>Nature</i> , 1999;402:83-86.
	X	Marcotte, E.M., "Computational genetics: finding protein function by nonhomology methods," <i>Curr Opin. Struct. Biol.</i> , 2000;10:359-365.
	X	Martelli et al., "A sequence-profile-based HMM for predicting and discriminating beta barrel membrane proteins," <i>Bioinformatics</i> , 2002;18: S46-53.
	X	Mathura et al., "Identifying Property Based Sequence Motifs in Protein Families and Superfamilies: Application to DNase I related endonucleases," <i>Bioinformatics</i> , 2003;19(11):1381-1390.
	X	Mathura et al., "Automated Generation of Property Based Motifs to Search for Functional Neighbors and to Improve Sequence Alignments," <i>5th Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, CASP5</i> , Asilomar Conference Center, Pacific Grove, CA, December 1-5, 2002: A-178-179.
	X	Mathura et al., "Identifying Property Based Sequence Motifs in Protein Families and Superfamilies: Application to APE," <i>2002 Bioinformatics Symposium</i> , Rice University, Houston, TX, October 14-15, 2002: 37.
	X	Mathura et al., "Defining Physical-chemical Properties based motifs specific for members of the APE family of DNA repair proteins," <i>7th Structural Biology Symposium</i> , UTMB, Galveston, TX, May 17-19, 2002:93.
	X	Mathura et al., "Sequence and Structural Analysis of APE 1 Protein Family Using Physical-chemical Properties Based Motifs," <i>RECOMB, Currents in Computational Molecular Biology 2002</i> , Washington, DC.: 191-192.
	X	Mathura et al., "Physical-chemical properties based motifs for annotating protein sequences from genomic data," <i>Molecular Genomics 2002: Profiling of Gene Expression</i> , UTMB, Galveston, TX, April 5-7, 2002:35.
	X	Mathura et al., "Quantitative Descriptors for Amino Acids Based on Physico-Chemical Properties using Vector Representation," <i>Keck 2000 Symposium</i> , Baylor College of Medicine and Rice University, Houston, TX, October 16-17, 2000: 33.
	X	Mathura et al., "A New Vector Representation of Amino Acids Based on Large Number of Physico-Chemical Properties," <i>Fifth Annual Structural Biology Symposium</i> , UTMB, Galveston, TX, May 19-21, 2000: 54.
UK	X	Mehta et al., "Recognizing very distant sequence relationships among proteins by family profile analysis," <i>Proteins</i> , 1999;35:387-400.

EXAMINER Lucia Claw	Date Considered 11/21/07
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	X	Norin et al., "Structural proteomics: developments in structure-to-function predictions," <i>Trends Biotechnol.</i> , 2002;20:79-84.
	X	Overbeek et al., "The use of gene clusters to infer functional coupling," <i>Proc Natl Acad Sci USA</i> , 16 March 1999;96(6):2896-2901.
	X	Oezguen et al., "APE1: Identifying Motifs by MASIA and Metalion Position by MD-Simulations," <i>Keck Center 2001 Annual Research Conference</i> , Galveston, TX, September 21, 2001:35.
	X	Press et al., "Numerical Recipes in C: The Art of Scientific Computing," 1999, Cambridge University Press, New York.
	X	"Prosite Database of protein families and domains."[online]. Expasy Prosite.[retrieved on 2004-07-06]. Retrieved from the Internet.< http://us.expasy.org/prosite/ >;2 pgs.
	X	Rigoutsos et al., "Dictionary-driven protein annotation," <i>Nucleic Acids Res</i> , 2002;30:3901-3916.
	X	Rison et al., "Comparison of functional annotation schemes for genomes," <i>Funct Integr. Genomics</i> , 2000;1:56-69.
	X	Rychlewski et al., "Comparison of sequence profiles. Strategies for structural predictions using sequence information," <i>Protein Sci</i> , 2000;9:232-241.
	X	Schaffer et al., "IMPALA: matching a protein sequence against a collection of PSI-BLAST-constructed position-specific score matrices," <i>Bioinformatics</i> , 1999;16:1000-1011.
	X	Schaffer et al., "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements," <i>Nucleic Acids Res</i> , 2001;29:2994-3005.
	X	Schein et al., "Total sequence decomposition distinguishes functional modules, "molegos" in apurinic/apyrimidinic endonucleases," <i>BMC Bioinformatics</i> , 2002;3:37.
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	X	Schein et al., "Defining the mode of action of APE1 using MASIA motif searching, MD-simulations and site directed mutagenesis," <i>6th Annual Structural Biology Symposium</i> , UTMB Galveston, TX, May 18-20, 2001: 83.
	X	Truong et al., "Identification and characterization of subfamily-specific signature in a large protein superfamily by a hidden Markov model approach," <i>BMC Bioinformatics</i> , 2002;3(1).
	X	Urushihara, H., "Functional genomics of the social amoebae, Dictyostelium discoideum," <i>Mol. Cell</i> , 2002;13:1-4.
	X	Venkatarajan et al., "New quantitative descriptors of amino acids based on multidimensional scaling of a large number of physical -chemical properties," <i>J Mol Model</i> , 2001;7:445-453.
	X	Waterston et al., "On the sequencing of the human genome," <i>Proc. Natl. Acad. Sci USA</i> , 2002;99(6):3712-3716.
	X	Yona et al., "Within the twilight zone: a sensitive profile-profile comparison tool based on information theory," <i>J Mol Biol.</i> , 2002;315: 1257-1275.
✓ LAC	X	Zhu et al., "MASIA: recognition of common patterns and properties in multiple aligned protein sequences," <i>Bioinformatics</i> , 2000;16:950-951.
EE		

EXAMINER Jon A. C.	Date Considered 11/21/07
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FOREIGN PATENT DOCUMENTS

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							Yes	No
		None						

OTHER DOCUMENTS (Including Authors, Title, Date, Pertinent Papers, etc.)

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/LC/	X	Schein et al., "Molego-Based Definition of the Architecture and Specificity of Metal-Binding Sites," <i>PROTEINS: Structure, Function, and Bioinformatics</i> , 2005; 58:200-210.
/LC/	X	Schein et al., "Stereophysicochemical variability plots highlight conserved antigenic areas in Flaviviruses," <i>Virology Journal</i> , April 2005; 2:40.

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